

A new *Ilarvirus* found in rose

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Rose rosette, a devastating disease in the midwestern and southeastern United States, is vectored by the eriophyoid mite *Phyllocoptes fructiphilus*, and the causal agent is believed to be a virus (Ahn *et al.*, 1996). In an attempt to characterize the causal agent of the disease, double-stranded RNA (dsRNA) was isolated from diseased plants. One of the plants assayed gave a dsRNA band pattern similar to that of viruses in the *Bromoviridae* family. DsRNA was cloned as described (Tzanetakis *et al.*, 2005) and several clones were sequenced to determine the origin of the bands. Sequence analysis indicated that a new virus can infect rose. The novel virus, named hereafter Rose virus 1 (RsV-1), shared about 70% nucleotide identities with *Strawberry necrotic shock virus* (SNSV) and *Tobacco streak virus* (TSV) and less than 50% identities with the other two rose-infecting ilarviruses, *Prunus necrotic ringspot virus* and *Apple mosaic virus*. Regions of RsV-1 RNA 1 (591 bp) and 3 (1202 bp) have been deposited in GenBank under accession numbers DQ329377 and DQ329378, respectively.

Primers F (5'-GTTTCCTGTGCTCCTCA-3') and R (5'-GTCACAC-CGAGGTACT-3') were developed for RT-PCR detection of RsV-1. The primers amplified a 519-base fragment of RNA 3 and were used on both total RNA and dsRNA templates. Amplicons obtained from both templates were sequenced and were RsV-1-specific. However RsV-1 does not appear to be the causal agent of rose rosette, as the virus was not detected by RT-PCR in dsRNA extracts made from other plants with rose rosette. This finding is in agreement with previous observations on this disease (Ahn *et al.*, 1996).

The detection protocol can be employed in rose virus certification schemes and surveys, while further work is needed in order to identify the

possible involvement of the virus in rose and rosaceous host diseases, in a similar situation to that identified in *Rubus* and *Fragaria* species with TSV and SNSV (Tzanetakis *et al.*, 2004).

While this report was under review, sequence of a novel virus from blackberry, Blackberry chlorotic ringspot virus (BCRV), was released in GenBank (accession numbers DQ091193-5; Jones *et al.* 2006); S. W. Scott, personal communication). The two viruses share 85–90% nucleotide identity (85–93% amino acid identity) and should therefore be considered strains of the same virus. For simplicity reasons, RsV-1 was renamed to BCRV in GenBank.

References

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